

AMENDMENTS TO THE SPECIFICATION

The following paragraph will replace the previous paragraph at page 4 located at paragraph 6:

PFAM (protein families database of alignments and hidden Markov models; <http://www.sanger.ac.uk/Software/Pfam/>) represents a large collection of protein sequence alignments. Each PFAM makes it possible to visualize multiple alignments, see protein domains, evaluate distribution among organisms, gain access to other databases, and visualize known protein structures.

The following paragraph will replace the previous paragraph located at page 4 at paragraph 7:

COGs (clusters of orthologous groups of proteins; <http://www.ncbi.nlm.nih.gov/COG/>) are obtained by comparing protein sequences from 43 fully sequenced genomes representing 30 major phylogenic lines. Each COG is defined from at least three lines, which permits the identification of former conserved domains.

The following paragraph will replace the previous paragraph located at page 4 continuing on page 5 at paragraph 8:

The means of identifying homologous sequences and their percentage homologies are well known to those skilled in the art, and include in particular the BLAST programs, ~~which can be used from the website <http://www.ncbi.nlm.nih.gov/BLAST/> with the default parameters indicated on that website.~~ The sequences obtained can then be exploited (e.g., aligned) using, for example, the programs CLUSTALW (<http://www.ebi.ac.uk/clustalw/>) or MULTALIN (<http://prodes.toulouse.inra.fr/multalin/cgi-bin/multalin.pl>), with the default parameters indicated on those websites.

The following paragraph will replace the previous paragraph located at page 32 at paragraph 2:

Two oligonucleotides were used to implement this strategy:

- DmetER with 100 bases (SEQ ID NO 1):

tatccccgacgcaagttctgcgccgcctgcaccatgttcgccagtccgcgggtttctgccaccgcgcgtttcagCAT
ATGAATATCCTCCTTAG

with:

- a region (lower case) homologous to the sequence (4012903 to 4012824) of the gene *metE* (sequence 4010643 to 4012904, the reference sequence on the website <http://genolist.pasteur.fr/Colibri/>);

The following paragraph will replace the previous paragraph located at page 41 at paragraph 2:

For *metC*:

- DmetCR with 100 bases (SEQ ID NO 13):

ccggcggtccagatcggcaatcagatcgatctccagaccaatgcaggcgaaatcaagggtccgctaaaatcgatCA
TATGAATATCCTCCTTAG

with

- a region (lower case) homologous to the sequence (3151419 to 3151359) of the gene *metC* (sequence 3150251 to 3151438, reference sequence on the website <http://genolist.pasteur.fr/Colibri/>),

- a region (upper case) for the amplification of the chloramphenicol resistance cassette (reference sequence in Datsenko, K.A. & Wanner, B.L., 2000, PNAS, 97: 6640-6645),

- DmetCF with 100 bases (SEQ ID NO 14):

cggacaaaaagcttgatactcaactggtgaatgcaggacgcagcaaaaaatacactctcggcgcggtaaatagcgtgattTG
TAGGCTGGAGCTGCTTCG

with

- a region (lower case) homologous to the sequence (3150255 to 3150334) of the gene *metC*

- a region (upper case) for the amplification of the chloramphenicol resistance cassette.

The following paragraph will replace the previous paragraph located at page 43 at paragraph 2:

For *metBJ*:

- MetJR with 30 bases (SEQ ID NO 9):

ggtacagaaaccagcaggctgaggatcagc

homologous to the sequence (4125431 to 4125460) downstream of the gene *metJ* (sequence 4125975 to 4125581, reference sequence on the website <http://genolist.pasteur.fr/Colibri/>).

The following paragraph will replace the previous paragraph located at page 44 at paragraph 3:

To delete the gene *metC* (sequence 3150251 to 3151438, the reference sequence on the website <http://genolist.pasteur.fr/Colibri/>) of the strain MG1655 ($\Delta metB-\Delta metJ$), the method of phage P1 transduction is used. The protocol followed is implemented in 2 steps with the preparation of the phage lysate on the strain MG1655 $\Delta(metC::Cm)$ and then transduction into strain MG1655 $\Delta(metB-\Delta metJ)$.

The following paragraph will replace the previous paragraph located at page 49 at paragraph 2:

For *cysK*:

DcysKR with 100 bases (SEQ ID NO 15):

TgtgtcaattctttctcgtgaagatcgcgcaacaatgcggtgcttaataacgctcaccccgatgatggtagaataacCATATGAA
TATCCTCCTTAG

with

- a region (lower case) homologous to the sequence (2531396 to 2531317) of the gene *cysK* (reference sequence on the website <http://genolist.pasteur.fr/Colibri/>),
- a region (upper case) for the amplification of the chloramphenicol resistance cassette (reference sequence in Datsenko, K.A. & Wanner, B.L., 2000, PNAS, 97: 6640-6645).

The following paragraph will replace the previous paragraph located at page 50 at paragraph 1:

Pour *cysM*:

DcysMR with 100 bases (SEQ ID NO 17):

cccgcaccttgctctaaatgctctccccaaacaccccggtagaaggtagcgatcgccacgatcgagatgatcgccacCATATG
AATATCCTCCTTAG

with:

- a region (lower case) homologous to the sequence (2536699 to 2536778) of the gene *cysM* (reference sequence on the website <http://genolist.pasteur.fr/Colibri/>),
- a region (upper case) for the amplification of the kanamycin resistance cassette.
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The following paragraph will replace the previous paragraph located at page 54 at paragraph 2:

For this purpose two oligonucleotides are synthesized:

- DudhAR with 100 bases (SEQ ID NO 25):

cccgagatctctttgtttcccgatggaacaaaatttcagcgtgccacgttcacgacgattgtgcggtgccagTGTA
GGCTGGAGCTGCTTCG

with

- a region (lower case) homologous to the sequence (4157144 to 4157223) of the gene *udhA* (sequence 4158303 to 4156969, reference sequence on the website <http://genolist.pasteur.fr/Colibri/>),
- a region (upper case) for the amplification of the kanamycin resistance cassette (reference sequence in Datsenko, K.A. & Wanner, B.L., 2000, PNAS, 97: 6640-6645).

The following paragraph will replace the previous paragraph located at page 55 at paragraph 2:

For this purpose two oligonucleotides are synthesized:

- DpgiR with 100 bases (SEQ ID NO 29):

gcgccagcgtttatagcggttaacagaccattggtcgagctatcgtggctgctgattctttatcatcttcagctctgCATATG
AATATCCTCCTTAG

with

- a region (lower case) homologous to the sequence (4232980 to 4232901) of the gene *pgi* (sequence 4231337 to 4232986, reference sequence on the website <http://genolist.pasteur.fr/Colibri/>),
- a region (upper case) for the amplification of the chloramphenicol resistance cassette (reference sequence in Datsenko, K.A. & Wanner, B.L., 2000, PNAS, 97: 6640-6645).

The following paragraph will replace the previous paragraph located at page 57 at paragraph 1:

For this purpose two oligonucleotides are synthesized:

- DpfkAR with 100 bases (SEQ ID NO 33):

ttcgcgcagtcacgacgtcaccttgaacggagcgttcatttcgatagcgtcgaatgatgtcgtggtgaaccagctgCATA
TGAATATCCTCCTTAG

with

- a region (lower case) homologous to the sequence (4106081 to 4106002) of the gene *pfkA* (sequence 4105132 to 4106094, reference sequence on the website <http://genolist.pasteur.fr/Colibri/>),
- a region (upper case) for the amplification of the chloramphenicol resistance cassette (reference sequence in Datsenko, K.A. & Wanner, B.L., 2000, PNAS, 97: 6640-6645).

The following paragraph will replace the previous paragraph located at page 58 at paragraph 3:

For this purpose two oligonucleotides are synthesized:

- DpfbkBR with 100 bases (SEQ ID NO 37):
gcgggaaaggtaagcgtaaattttgcgtatcgtcatgggagcacagacgtgttcctgattgagtggtgctgcactccCATA
TGAATATCCTCCTTAG
with
- a region (lower case) homologous to the sequence (1805320 to 1805241) of the gene *pfkB* (sequence 1804394 to 1805323, reference sequence on the website <http://genolist.pasteur.fr/Colibri/>),
- a region (upper case) for the amplification of the chloramphenicol resistance cassette (reference sequence in Datsenko, K.A. & Wanner, B.L., 2000, PNAS, 97: 6640-6645).